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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:53:22 ; Search time 29 seconds

(without alignments)  
362.196 Million cell updates/sec

Title: US-09-997-585-399

Perfect score: 656

Sequence: 1 MLPALPALVFTVAMSLA.....SAQLCCMPVGARGALCQ 120

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:\*

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6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backffile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	656	100.0	120	2	US-09-997-333-399
4	656	100.0	120	2	US-09-992-558-399
5	656	100.0	120	2	US-09-989-735-399
6	656	100.0	120	3	US-09-989-726-399
7	656	100.0	120	3	US-09-997-514-399
8	656	100.0	120	3	US-09-989-728-399
9	656	100.0	120	3	US-09-997-349-399
10	656	100.0	120	3	US-09-997-653-399
11	656	100.0	120	3	US-09-989-293A-399
12	656	100.0	120	3	US-09-992-991A-25768
13	656	100.0	120	3	US-09-949-016-10974
14	656	100.0	120	3	US-09-489-039A-8252
15	656	100.0	120	3	US-09-701-868-8
16	656	100.0	120	3	US-08-696-944-19
17	656	100.0	120	3	US-09-958-359-19
18	656	100.0	120	3	US-09-489-039A-9684
19	656	100.0	120	3	US-09-413-814-11
20	656	100.0	120	3	US-09-252-991A-21618
21	656	100.0	120	3	US-09-252-991A-30876
22	656	100.0	120	3	US-09-252-991A-20640
23	656	100.0	120	3	US-09-252-991A-19607
24	656	100.0	120	3	US-09-252-991A-27893
25	656	100.0	120	3	US-09-252-991A-26217
26	656	100.0	120	3	US-09-205-258-608

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28	69.5	10.6	283	2	US-09-450-209-14	Sequence 14, Appli
29	69.5	10.6	738	2	US-08-989-395-1	Sequence 1, Appli
30	69.5	10.6	738	2	US-09-593-826-1	Sequence 1, Appli
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33	69.5	10.6	1461	3	US-10-142-231-86	Sequence 86, Appl
34	69.5	10.6	1461	3	US-10-884-115-86	Sequence 86, Appl
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36	69	10.5	485	2	US-09-489-039A-10866	Sequence 10866, A
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59	67	10.2	158	2	US-08-826-134-22	Sequence 22, Appl
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98	63.5	9.7	291	3	US-10-829-107-5	Sequence 5, Appli
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103	63	9.6	154	US-10-094-749-1759	Sequence 1759, Ap	176	60	9.1	144	US-09-252-991A-16888	Sequence 16888, A
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105	63	9.6	280	US-09-758-759-192	Sequence 192, App	178	60	9.1	195	US-09-489-847-138	Sequence 338, App
106	63	9.6	412	US-09-027-064-4	Sequence 4, Appl1	179	60	9.1	199	PCT-US93-10418-4	Sequence 4, Appl1
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111	63	9.6	475	US-09-323-433A-14	Sequence 14, Appl	184	60	9.1	296	US-09-116-622-6	Sequence 6, Appl1
112	63	9.6	475	US-09-826-752-14	Sequence 14, Appl	185	60	9.1	296	US-09-219-277-6	Sequence 6, Appl1
113	63	9.6	681	US-09-252-991A-24159	Sequence 24159, A	186	60	9.1	296	US-09-599-661-6	Sequence 6, Appl1
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115	62.5	9.5	190	US-08-044-621D-28	Sequence 28, Appl	188	60	9.1	315	US-09-904-615-124	Sequence 124, App
116	62.5	9.5	190	US-08-709-912-14	Sequence 14, Appl	189	60	9.1	315	US-10-054-988-124	Sequence 124, App
117	62.5	9.5	190	US-09-047-370-14	Sequence 14, Appl	190	60	9.1	344	US-10-037-417-4-4	Sequence 44, Appl
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125	62	9.5	102	US-09-702-705-1675	Sequence 1675, Ap	198	60	9.1	993	US-10-237-521-50	Sequence 50, Appl
126	62	9.5	102	US-09-736-457-1675	Sequence 1675, Ap	199	60	9.1	1037	US-09-894-998A-54	Sequence 54, Appl
127	62	9.5	102	US-09-671-325-1675	Sequence 1675, Ap	200	60	9.1	1037	US-10-237-551-54	Sequence 54, Appl
128	62	9.5	102	US-09-658-824-1675	Sequence 1675, Ap	201	60	9.1	1113	US-09-894-998A-51	Sequence 51, Appl
129	62	9.5	102	US-10-017-754-1675	Sequence 1675, Ap	202	60	9.1	1113	US-10-237-551-51	Sequence 51, Appl
130	62	9.5	102	US-09-651-563-1675	Sequence 1675, Ap	203	60	9.1	1114	US-10-237-551-102	Sequence 202, App
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135	62	9.5	545	US-09-514-242-2	Sequence 2, Appl1	208	59.5	9.1	185	US-09-047-370-3	Sequence 3, Appl1
136	62	9.5	1235	US-09-949-016-8455	Sequence 8455, Ap	209	59.5	9.1	185	US-09-570-856B-4	Sequence 4, Appl1
137	62	9.5	1235	US-09-949-016-8456	Sequence 8456, Ap	210	59.5	9.1	185	US-09-570-856B-5	Sequence 5, Appl1
138	62	9.5	2169	US-09-949-016-6930	Sequence 6930, Ap	211	59.5	9.1	185	US-09-570-856B-6	Sequence 6, Appl1
139	61.5	9.4	116	US-08-428-197-10	Sequence 10, Appl	212	59.5	9.1	185	US-09-570-856B-7	Sequence 7, Appl1
140	61.5	9.4	116	PCT-US93-10555-10	Sequence 10, Appl	213	59.5	9.1	185	US-09-570-856B-8	Sequence 8, Appl1
141	61.5	9.4	223	US-09-254-723-7	Sequence 7, Appl1	214	59.5	9.1	185	US-09-570-856B-9	Sequence 9, Appl1
142	61.5	9.4	245	US-10-104-047-3466	Sequence 3466, Ap	215	59.5	9.1	185	US-09-570-856B-10	Sequence 10, Appl
143	61.5	9.4	532	US-09-252-991A-22039	Sequence 22039, A	216	59.5	9.1	185	US-09-252-991A-20667	Sequence 20667, A
144	61.5	9.4	654	US-09-252-991A-25801	Sequence 25801, A	217	59.5	9.1	187	US-09-252-991A-28935	Sequence 28935, A
145	61.5	9.4	1441	US-09-252-991A-28143	Sequence 28143, A	218	59.5	9.1	188	US-08-044-621D-26	Sequence 26, Appl
146	61.5	9.4	3461	US-09-334-220-2	Sequence 2, Appl1	219	59.5	9.1	190	US-08-044-621D-27	Sequence 27, Appl
147	61	9.3	147	US-09-252-991A-24662	Sequence 24662, A	220	59.5	9.1	190	US-08-709-912-16	Sequence 16, Appl
148	61	9.3	239	US-09-252-991A-24294	Sequence 24294, A	221	59.5	9.1	190	US-08-709-912-17	Sequence 17, Appl
149	61	9.3	376	US-09-290-586A-23	Sequence 23, Appl	222	59.5	9.1	190	US-09-047-370-16	Sequence 16, Appl
150	61	9.3	393	US-09-784-077-2	Sequence 2, Appl1	223	59.5	9.1	190	US-09-047-370-17	Sequence 17, Appl
151	61	9.3	441	US-09-328-352-5065	Sequence 5065, Ap	224	59.5	9.1	190	US-09-570-856B-19	Sequence 19, Appl
152	61	9.3	597	US-09-883-524-6	Sequence 6, Appl1	225	59.5	9.1	190	US-09-570-856B-22	Sequence 22, Appl
153	61	9.3	597	US-09-204-764-6	Sequence 21, Appl	226	59.5	9.1	190	US-09-570-856B-21	Sequence 21, Appl
154	61	9.3	614	PCT-US95-0326-21	Sequence 21, Appl	227	59.5	9.1	208	US-08-315-605-21	Sequence 21, Appl
155	61	9.3	1572	US-09-710-279-2506	Sequence 2906, Ap	228	59.5	9.1	213	US-09-570-856B-13	Sequence 13, Appl
156	61	9.3	3907	US-10-029-217A-24	Sequence 24, Appl	229	59.5	9.1	223	US-08-121-436A-2	Sequence 2, Appl1
157	60.5	9.2	118	US-09-489-039A-8080	Sequence 8080, Ap	230	59.5	9.1	223	US-08-315-605-18	Sequence 18, Appl
158	60.5	9.2	119	US-10-268-883-3	Sequence 3, Appl1	231	59.5	9.1	369	US-09-248-796A-15604	Sequence 15604, A
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164	60.5	9.2	232	US-09-252-991A-21812	Sequence 21812, A	237	59.5	9.1	1733	US-09-958-359-21	Sequence 21, Appl
165	60.5	9.2	310	US-09-408-020-44	Sequence 44, Appl	238	59.5	9.1	96	US-08-241-853-20	Sequence 20, Appl
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167	60.5	9.2	393	US-09-107-532A-6470	Sequence 6470, Ap	240	59	9.0	123	US-08-840-459-94	Sequence 94, Appl
168	60.5	9.2	391	US-09-489-039A-13161	Sequence 13161, A	241	59	9.0	123	US-09-497-625A-94	Sequence 94, Appl
169	60.5	9.2	438	US-09-591-279A-41	Sequence 41, Appl	242	59	9.0	140	US-09-270-767-15666	Sequence 35666, A
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171	60.5	9.2	516	US-09-902-540-10341	Sequence 10341, A	244	59	9.0	140	US-09-270-767-15666	Sequence 50903, A
172	60.5	9.2	522	US-10-026-106E-8	Sequence 8, Appl1	245	59	9.0	261	US-08-927-219-55	Sequence 55, Appl

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:53:37 ; Search time 40 Seconds  
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288.650 Million cell updates/sec

Title: US-09-997-585-399

Perfect score: 656  
Sequence: 1 MLPALPPALVFTVMSLLA.....SAQLLCMPGVNAGALCO 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

Database :

1: PIR.80.\*  
2: PIR1.\*  
3: PIR2.\*  
4: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	12.7	502	2 T36589	probable transmemb
2	77.5	11.8	432	2 A70714	hypothetical prote
3	76.5	11.7	113	2 A34792	Ig heavy chain pre
4	76	11.6	1133	2 A54164	sterol regulatory
5	75.5	11.5	368	2 T44887	probable branched-
6	74.5	11.4	835	2 T06590	probable beta-gala
7	73	11.1	224	2 A13021	two component resp
8	73	11.1	244	2 A98263	transcription regu
9	72.5	11.1	3104	2 S20473	fatty-acid synthas
10	72	11.0	159	2 B83245	hypothetical prote
11	72	11.0	1063	2 A40253	acidic nuclear pro
12	71.5	10.9	236	2 T36188	hypothetical prote
13	71	10.8	210	2 B75450	hypothetical prote
14	71	10.8	342	2 AD0346	probable transport
15	70.5	10.7	368	2 C70786	probable live prot
16	70.5	10.7	456	2 T06136	aspartate transami
17	70.5	10.7	591	2 P83472	aspartate transami
18	70	10.7	321	2 AB1054	probable glycosyl
19	70	10.7	478	2 C87351	probable membrane
20	69.5	10.6	345	2 T35357	aldehyde dehydroge
21	69.5	10.6	418	2 S46315	hypothetical prote
22	69.5	10.6	535	2 P70782	aspartate transami
23	69	10.5	392	2 T35487	probable oxidoredu
24	69	10.5	893	2 H95953	hypothetical prote
25	69	10.5	1234	2 A84310	probable biluncio
26	68.5	10.4	140	2 S54240	cobalamin biosynth
27	68	10.4	581	2 G70189	Ig mu heavy chain
28	68	10.4	592	2 D70863	threonine-tRNA lig
29	67.5	10.3	312	2 C75377	hypothetical prote
					probable glucose 6

30	67.5	10.3	420	2 T08005	flavonol 3-O-glucos
31	67	10.2	264	2 E72642	hypothetical prote
32	67	10.2	1381	2 T31083	parandoin - rat
33	67	10.2	1385	2 T14158	neurixin IV - mous
34	66.5	10.1	115	2 S19665	Ig heavy chain V r
35	66.5	10.1	355	2 C85552	phosphoribosylam
36	66.5	10.1	355	2 E90701	phosphoribosylam
37	66.5	10.1	1019	2 AB2136	polyketide synthas
38	66.5	10.1	1154	2 S43275	hypothetical prote
39	66.5	10.1	1339	2 T47841	hypothetical prote
40	66	10.1	154	2 AB0116	methyglyoxal synt
41	66	10.1	218	2 H70856	hypothetical prote
42	65.5	10.0	101	2 E72698	hypothetical prote
43	65.5	10.0	201	2 T07729	wound-induced prot
44	65.5	10.0	231	2 S77323	hypothetical prote
45	65.5	10.0	235	2 AB0114	deoxyribonuclease
46	65.5	10.0	266	1 TLBP2X	tail fiber protein
47	65.5	10.0	304	2 T37060	hypothetical prote
48	65.5	10.0	427	2 JC4915	age protein precu
49	65.5	10.0	468	2 B70932	probable PPG prote
50	65.5	10.0	1827	2 B70984	probable polyketid
51	65	9.9	352	2 A25466	photoactiveem II pro
52	65	9.9	357	2 T33507	hypothetical prote
53	65	9.9	368	2 G86416	hypothetical prote
54	65	9.9	2090	2 T30075	hypothetical prote
55	65	9.9	2153	2 T30074	hypothetical prote
56	64.5	9.8	238	2 D95968	conserved hypotnet
57	64.5	9.8	424	2 S09884	hypothetical prote
58	64.5	9.8	883	1 OYEC	phosphoenolpyruvat
59	64.5	9.8	883	2 B86087	phosphoenolpyruvat
60	64.5	9.8	883	2 E91239	phosphoenolpyruvat
61	64.5	9.8	1748	2 S42136	cnjB protein - Tet
62	64	9.8	120	2 UQ1740	hypothetical 12.7k
63	64	9.8	260	1 JS0635	rRNA (adenine-N6-)
64	64	9.8	564	2 H86278	phosphoenolpyruvat
65	64	9.8	619	2 A45625	probable aldehyde
66	64	9.8	746	2 F95890	glycogen phosphory
67	64	9.8	847	1 A25518	genome polypoteain
68	64	9.8	2183	1 GNN1B4	hepatic lectin H1
69	63.5	9.7	291	1 LNNH1	phosphoribosylam
70	63.5	9.7	355	1 DCECPK	aspartate transami
71	63.5	9.7	449	2 T48511	probable fructuron
72	63.5	9.7	486	2 A64909	probable oxidoredu
73	63.5	9.7	486	2 H85719	related to stress
74	63.5	9.7	486	2 G90897	probable oxidoredu
75	63.5	9.7	618	2 T49741	PFAT2 protein - hu
76	63	9.6	233	2 JC7618	glutaryl-CoA dehyd
77	63	9.6	395	2 G69373	probable membrane
78	63	9.6	475	2 S49886	hypothetical prote
79	63	9.6	488	2 T19884	endo-1,4-beta-xyla
80	62.5	9.5	190	1 A44593	hypothetical prote
81	62.5	9.5	318	2 G84143	angiotensin precu
82	62.5	9.5	476	1 JC2318	hypothetical prote
83	62.5	9.5	561	2 D84800	probable propionyl
84	62.5	9.5	628	2 D90677	probable propionyl
85	62.5	9.5	628	2 G85527	probable phosphodi
86	62.5	9.5	746	2 T35811	phosphoenolpyruvat
87	62.5	9.5	883	2 AD0936	transcription acti
88	62.5	9.5	1442	2 T42607	conserved hypotnet
89	62	9.5	140	2 AE3007	hypothetical prote
90	62	9.5	160	2 A96277	conserved hypotnet
91	62	9.5	160	2 AC2799	phox2 homeodomain
92	62	9.5	280	2 I48713	probable dioxigena
93	62	9.5	382	2 G70946	related to GTP-Din
94	62	9.5	402	2 T52356	hypothetical prote
95	62	9.5	706	2 E86143	probable DNA misma
96	62	9.5	766	2 A75332	hypothetical prote
97	62	9.5	1321	2 T00382	Cdh peptide synthe
98	62	9.5	3670	2 T36249	related to Immedia
99	61.5	9.4	218	2 T49680	3a protein - peanu
100	61.5	9.4	282	1 P3VXPS	probable CELF DivI
101	61.5	9.4	337	2 T52358	aspartyl proteinas
102	61.5	9.4	398	2 A36926	

103	61.5	9.4	407	2	JCS124	aspartate transami	176	59.5	9.1	646	2	D82493	conserved hypot
104	61.5	9.4	426	2	B71408	probable acylamino	177	59.5	9.1	954	1	S20907	endo-1,4-beta-xyla
105	61.5	9.4	441	2	A83370	probable MFS trans	178	59.5	9.1	959	2	E85276	hypothetical prote
106	61.5	9.4	764	2	JC8016	acylaminoacyl-pept	179	59.5	9.1	1376	2	F72609	probable reverse g
107	61.5	9.4	1417	2	H83132	probable sensor/re	180	59.5	9.1	2610	2	T20968	hypothetical prote
108	61.5	9.4	3461	2	S58870	reelin precursor -	181	59.5	9.0	123	2	A36060	Ig heavy chain V r
109	61	9.3	115	2	T51208	hypothetical prote	182	59	9.0	238	2	A80006	tRNA nucleotidyltr
110	61	9.3	260	2	S49386	capsid protein V2	183	59	9.0	241	1	S35322	crystallin beta B1
111	61	9.3	312	2	C75561	conserved hypotet	184	59	9.0	260	1	VCCWV	coat protein - whe
112	61	9.3	435	2	AF2079	hypothetical prote	185	59	9.0	296	6	A87000	probable chloisula
113	61	9.3	450	2	AD0522	probable exported	186	59	9.0	307	2	F71294	hypothetical prote
114	61	9.3	570	1	A45591	hemagglutinin prec	187	59	9.0	365	2	A47046	cobalt/zinc/cadmiu
115	61	9.3	614	2	A25707	UI snRNP 70K prote	188	59	9.0	369	2	C65497	probable fibribria
116	61	9.3	632	2	C86922	probable membrane	189	59	9.0	369	2	C90646	probable fibribria
117	61	9.3	850	2	S22338	glycogen phosphory	190	59	9.0	413	2	S01076	aspartate transami
118	61	9.3	2706	2	T28155	variant-specific B	191	59	9.0	477	2	H70747	probable ammonium
119	60.5	9.2	209	2	JC4909	endo-1,4-beta-xyla	192	59	9.0	479	2	G82114	sigma-54 dependent
120	60.5	9.2	235	2	AB0877	endonuclease I [lm	193	59	9.0	485	2	G71239	hypothetical prote
121	60.5	9.2	261	1	WMBEXE	infected cell prot	194	59	9.0	538	2	T40992	hypothetical prote
122	60.5	9.2	342	2	H86336	hypothetical prote	195	59	9.0	570	2	S22013	hemagglutinin prec
123	60.5	9.2	346	2	H85057	probable transposo	196	59	9.0	570	2	S22017	hemagglutinin prec
124	60.5	9.2	438	2	B70779	probable kasb prot	197	59	9.0	672	2	T36083	hypothetical prote
125	60.5	9.2	487	2	S61243	deoxyribonuclease	198	59	9.0	953	2	S56650	pyruvate, phosphat
126	60.5	9.2	509	2	JCS055	high affinity nitr	199	59	9.0	953	2	S12894	pyruvate, phosphat
127	60.5	9.2	509	2	G83442	probable 3-hydroxy	200	59	9.0	1075	2	T48805	hypothetical prote
128	60.5	9.2	572	2	T34658	hypothetical prote	201	59	9.0	1309	2	T00078	probable RNA-dirc
129	60.5	9.2	572	2	AF3068	two component sens	202	59	9.0	1677	2	T14267	Xin protein, stage
130	60.5	9.2	579	2	E98218	exsg protein (A)22	203	59	9.0	1897	1	TDHULK	leukocyte antigen-
131	60.5	9.2	643	2	H64119	chroline-tRNA lig	204	58.5	8.9	120	2	B72519	hypothetical prote
132	60.5	9.2	825	2	H64083	biclin sulfoxide r	205	58.5	8.9	210	2	G83762	endo-1,4-beta-xyla
133	60.5	9.2	935	2	E96806	hypothetical prote	206	58.5	8.9	248	2	A81040	conserved hypotet
134	60.5	9.2	1230	2	E64664	outer membrane pro	207	58.5	8.9	248	2	S56531	hypothetical 27.4K
135	60.5	9.2	1237	2	D71850	probable outer mem	208	58.5	8.9	321	2	B87658	hypothetical prote
136	60	9.1	80	2	E83102	conserved hypotet	209	58.5	8.9	342	2	S14432	heterogeneous ribo
137	60	9.1	135	2	T01322	aluminum-induced p	210	58.5	8.9	379	2	S41329	phosphoserine amin
138	60	9.1	257	2	A83362	env polypeptin -	211	58.5	8.9	409	2	S41329	5-enoilpyruvylshik
139	60	9.1	283	2	C83248	hypothetical prote	212	58.5	8.9	415	2	T02377	hypothetical prote
140	60	9.1	378	2	AF3320	flavohemoprotein l	213	58.5	8.9	434	2	G83129	probable MFS trans
141	60	9.1	381	2	G70626	hypothetical prote	214	58.5	8.9	469	2	E86421	hypothetical prote
142	60	9.1	398	2	G82755	conserved hypotet	215	58.5	8.9	534	2	F84398	phosphate ABC tran
143	60	9.1	410	2	T36610	hypothetical prote	216	58.5	8.9	591	2	D70562	hypothetical prote
144	60	9.1	484	2	B70586	probable amia2 pro	217	58.5	8.9	616	1	RRVOL	probable RNA-dirc
145	60	9.1	504	2	A84244	probable signaling	218	58.5	8.9	627	2	T35608	polyketide hydroxy
146	60	9.1	563	1	HMIYCV	hemagglutinin prec	219	58.5	8.9	649	2	H86920	probable membrane
147	60	9.1	672	1	S73438	MG032 homolog B01	220	58.5	8.9	666	2	B56639	1,4-alpha-glucan b
148	60	9.1	788	1	Q08BE3	HHLF1 protein - hu	221	58.5	8.9	712	1	YSHUT	threonine-tRNA lig
149	60	9.1	819	2	B87386	hypothetical prote	222	58.5	8.9	1570	2	AC2012	hypothetical prote
150	60	9.1	846	1	Q08EC3	HORP1 protein - hu	223	58.5	8.9	4302	2	A38971	polycystic kidney
151	60	9.1	947	2	H85088	hypothetical prote	224	58	8.8	112	2	T36440	hypothetical prote
152	60	9.1	1007	2	H72734	hypothetical prote	225	58	8.8	140	2	S54242	Ig mu heavy chain
153	60	9.1	1487	1	EDBBE1	immediate-early pr	226	58	8.8	221	2	A13631	hypothetical prote
154	60	9.1	1487	1	EDBBF6	155K transcripion	227	58	8.8	247	1	Q08BE1	HXLF3 protein prec
155	59.5	9.1	122	2	S30533	Ig heavy chain V r	228	58	8.8	270	2	E95034	bifunctional folat
156	59.5	9.1	168	2	C70824	probable transcrip	229	58	8.8	272	2	T41070	conserved hypotet
157	59.5	9.1	190	1	A44594	endo-1,4-beta-xyla	230	58	8.8	278	2	D75585	urase accessory p
158	59.5	9.1	213	1	A44594	endo-1,4-beta-xyla	231	58	8.8	328	2	T36200	probable DNA polym
159	59.5	9.1	230	1	I40569	endo-1,4-beta-xyla	232	58	8.8	335	2	F75103	6-phosphotrucokin
160	59.5	9.1	213	1	S01734	endo-1,4-beta-xyla	233	58	8.8	335	2	D57971	class I histocoma
161	59.5	9.1	213	1	S48126	endo-1,4-beta-xyla	234	58	8.8	355	2	B40730	class I histocoma
162	59.5	9.1	222	2	S31554	xylanase 1 - fungu	235	58	8.8	359	2	E83312	hypothetical prote
163	59.5	9.1	223	2	S39883	endo-1,4-beta-xyla	236	58	8.8	396	2	H87709	HLVD family secret
164	59.5	9.1	223	2	T16335	hypothetical prote	237	58	8.8	410	1	S78615	serine/chreonine/c
165	59.5	9.1	333	2	T33642	conserved hypotet	238	58	8.8	471	2	S78597	argininonuccinate
166	59.5	9.1	392	2	T01849	hypothetical prote	239	58	8.8	482	2	B83867	NADP-dependent gly
167	59.5	9.1	405	2	D81729	Mcr/TnaB/TyO perm	240	58	8.8	486	2	H83131	5-carboxy-2-hydrox
168	59.5	9.1	431	2	T14311	aspartate transami	241	58	8.8	606	2	T31552	WDRI protein - hum
169	59.5	9.1	409	2	S53303	aspartate transami	242	58	8.8	615	2	S54468	Arp1 protein - yea
170	59.5	9.1	412	1	XNCHDC	aspartate transami	243	58	8.8	700	2	G90885	hypothetical prote
171	59.5	9.1	413	1	XNPGDC	aspartate transami	244	58	8.8	700	2	F64897	probable tom-depe
172	59.5	9.1	503	2	H95390	probable reverse t	245	58	8.8	700	2	H85732	hypothetical prote
173	59.5	9.1	553	2	AH3191	canasee (imported)	246	58	8.8	748	2	T37097	probable secreted
174	59.5	9.1	564	2	AH2066	hypothetical prote	247	58	8.8	774	2	A28392	penicillin amidase
175	59.5	9.1	570	2	T20166	hypothetical prote	248	58	8.8	841	2	S34624	glycogen phosphory

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:59:53 ; Search time 18 Seconds

(without alignments)  
384.454 Million cell updates/sec

Perfect score: 656  
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Scoring table: BLOSUM62  
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Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications\_AA\_New:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.5	12.6	602	US-10-449-902-44709	Sequence 44709, A
2	74.5	11.4	160	US-11-056-355B-17946	Sequence 17946, A
3	74	11.3	505	US-10-449-902-38376	Sequence 38376, A
4	72	11.0	426	US-10-449-902-33556	Sequence 33556, A
5	70.5	10.7	419	US-10-953-349-16414	Sequence 16414, A
6	70.5	10.7	449	US-10-449-902-36203	Sequence 36203, A
7	70.5	10.7	456	US-10-953-349-16413	Sequence 16413, A
8	70	10.7	1665	US-11-174-307B-8696	Sequence 2696, Ap
9	69.5	10.6	247	US-11-056-355B-103232	Sequence 103232, A
10	69.5	10.6	247	US-11-056-355B-114471	Sequence 114471, A
11	69.5	10.6	262	US-11-056-355B-103231	Sequence 103231, A
12	69.5	10.6	262	US-11-056-355B-114470	Sequence 114470, A
13	69.5	10.6	258	US-11-174-307B-1572	Sequence 1572, Ap
14	69	10.5	995	US-10-449-902-40020	Sequence 40020, A
15	69	10.5	364	US-11-293-697-3925	Sequence 3925, Ap
16	68.5	10.4	222	US-10-953-349-25727	Sequence 25727, A
17	68.5	10.4	1744	US-11-174-307B-8750	Sequence 2750, Ap
18	68	10.4	512	US-10-449-902-43536	Sequence 43536, A
19	68	10.4	717	US-10-449-902-43536	Sequence 43536, A
20	67.5	10.3	119	US-11-056-355B-420	Sequence 420, App
21	67.5	10.3	180	US-11-293-697-4047	Sequence 4047, Ap
22	67.5	10.3	345	US-10-511-937-2562	Sequence 2562, Ap
23	67	10.2	1079	US-11-174-307B-4958	Sequence 4958, Ap
24	66.5	10.1	1170	US-11-174-307B-1988	Sequence 1988, Ap
25	66	10.1	1907	US-11-174-307B-2770	Sequence 2770, Ap
26	66	10.1	5109	US-11-174-307B-1520	Sequence 1520, Ap

27	65.5	10.0	195	US-11-056-355B-11294	Sequence 11294, A
28	65.5	10.0	255	US-11-056-355B-11293	Sequence 11293, A
29	65.5	10.0	1736	US-11-174-307B-2668	Sequence 2668, Ap
30	65	9.9	178	US-10-953-349-35149	Sequence 35149, A
31	65	9.9	1257	US-10-953-349-35148	Sequence 35148, A
32	65	9.9	1927	US-11-174-307B-24	Sequence 24, App1
33	65	9.9	1772	US-11-174-307B-4212	Sequence 4212, Ap
34	64.5	9.8	129	US-10-449-902-42109	Sequence 42109, A
35	64.5	9.8	254	US-11-075-891-6	Sequence 6, App1
36	64.5	9.8	254	US-11-075-891-8	Sequence 8, App1
37	64.5	9.8	254	US-11-075-891-12	Sequence 12, App1
38	64.5	9.8	254	US-11-075-891-14	Sequence 14, App1
39	64.5	9.8	254	US-11-075-891-18	Sequence 18, App1
40	64.5	9.8	254	US-11-075-891-20	Sequence 20, App1
41	64.5	9.8	274	US-11-056-355B-10952	Sequence 10952, A
42	64.5	9.8	282	US-10-953-349-34396	Sequence 34396, A
43	64.5	9.8	520	US-11-056-355B-100323	Sequence 100323, A
44	64.5	9.8	520	US-11-056-355B-111562	Sequence 111562, A
45	64.5	9.8	883	US-11-297-383-11	Sequence 11, App1
46	64.5	9.8	1376	US-11-174-307B-378	Sequence 378, App1
47	64.5	9.8	1379	US-11-174-307B-1738	Sequence 1738, Ap
48	64.5	9.8	1430	US-11-174-307B-982	Sequence 982, App
49	64.5	9.8	3723	US-11-174-307B-2802	Sequence 2802, App
50	64	9.8	793	US-10-449-902-54256	Sequence 54256, A
51	64	9.8	496	US-11-056-355B-72585	Sequence 72585, A
52	64	9.8	795	US-11-056-355B-72584	Sequence 72584, A
53	64	9.8	849	US-11-056-355B-72583	Sequence 72583, A
54	64	9.8	1073	US-10-449-902-50549	Sequence 50549, A
55	64	9.8	1933	US-11-174-307B-2226	Sequence 2226, Ap
56	64	9.8	161	US-11-174-307B-1618	Sequence 1618, Ap
57	63.5	9.7	322	US-10-449-902-16130	Sequence 16130, A
58	63.5	9.7	349	US-11-056-355B-16083	Sequence 16083, A
59	63.5	9.7	349	US-11-056-355B-16082	Sequence 16082, A
60	63.5	9.7	449	US-11-056-355B-36484	Sequence 36484, A
61	63.5	9.7	449	US-11-056-355B-104960	Sequence 104960, A
62	63.5	9.7	449	US-11-056-355B-116199	Sequence 116199, A
63	63.5	9.7	488	US-11-056-355B-16081	Sequence 16081, A
64	63.5	9.7	497	US-10-449-902-16453	Sequence 56453, A
65	63.5	9.7	693	US-10-449-902-19447	Sequence 49447, A
66	63.5	9.7	787	US-10-449-902-51130	Sequence 51130, A
67	63.5	9.7	1773	US-11-174-307B-2658	Sequence 2658, Ap
68	63.5	9.7	1779	US-11-174-307B-2160	Sequence 2160, Ap
69	63.5	9.7	1794	US-11-174-307B-2164	Sequence 2164, Ap
70	63.5	9.7	2499	US-11-174-307B-268	Sequence 268, App
71	63	9.6	233	US-11-289-102-344	Sequence 344, App
72	63	9.6	274	US-10-449-902-40249	Sequence 40249, A
73	63	9.6	319	US-11-056-355B-9046	Sequence 9046, Ap
74	63	9.6	394	US-10-449-902-18126	Sequence 48126, A
75	63	9.6	436	US-10-449-902-18174	Sequence 18174, A
76	63	9.6	483	US-10-449-902-16874	Sequence 46874, A
77	63	9.6	847	US-10-505-928-300	Sequence 300, App
78	63	9.6	1396	US-11-174-307B-466	Sequence 466, App
79	63	9.6	1486	US-11-174-307B-2552	Sequence 2552, Ap
80	63	9.6	1962	US-11-174-307B-1446	Sequence 1446, App
81	62.5	9.5	89	US-10-449-902-46974	Sequence 46974, A
82	62.5	9.5	324	US-11-056-355B-15943	Sequence 15943, A
83	62.5	9.5	344	US-10-449-902-23361	Sequence 53361, A
84	62.5	9.5	396	US-11-056-355B-115942	Sequence 115942, A
85	62.5	9.5	443	US-11-056-355B-18531	Sequence 85631, A
86	62.5	9.5	444	US-11-056-355B-85630	Sequence 85630, A
87	62.5	9.5	451	US-11-056-355B-15941	Sequence 15941, A
88	62.5	9.5	467	US-11-056-355B-15941	Sequence 15941, A
89	62.5	9.5	468	US-11-056-355B-70388	Sequence 70388, A
90	62.5	9.5	537	US-11-056-355B-70388	Sequence 70388, A
91	62.5	9.5	561	US-11-056-355B-85629	Sequence 85629, A
92	62.5	9.5	561	US-11-174-307B-34	Sequence 34, App1
93	62.5	9.5	561	US-11-056-355B-70387	Sequence 70387, A
94	62.5	9.5	1530	US-11-174-307B-1862	Sequence 1862, Ap
95	62.5	9.5	1821	US-11-174-307B-2108	Sequence 2108, App
96	62.5	9.5	2110	US-11-174-307B-2010	Sequence 2010, App
97	62	9.5	97	US-10-449-902-35088	Sequence 35088, A
98	62	9.5	102	US-10-449-902-48157	Sequence 48157, A
99	62	9.5	180	US-11-301-554-1675	Sequence 1675, Ap
			7	US-11-056-355B-2889	Sequence 2889, App

100	62	9.5	321	7	US-11-056-355B-6482	Sequence 6482, Ap	173	60	9.1	1863	7	US-11-174-307B-1830	Sequence 1830, Ap
101	62	9.5	340	7	US-11-056-355B-6481	Sequence 6481, Ap	174	60	9.1	2368	7	US-11-174-307B-2844	Sequence 2844, Ap
102	62	9.5	373	7	US-11-056-355B-6480	Sequence 6480, Ap	175	60	9.1	2391	7	US-11-174-307B-1386	Sequence 1386, Ap
103	62	9.5	706	7	US-11-056-355B-80144	Sequence 80144, A	176	60	9.1	2574	7	US-11-174-307B-1990	Sequence 1990, Ap
104	62	9.5	720	6	US-10-505-928-383	Sequence 383, App	177	60	9.1	3003	7	US-11-174-307B-228	Sequence 228, App
105	62	9.5	1393	7	US-11-174-307B-606	Sequence 606, App	178	60	9.1	3159	7	US-11-174-307B-1916	Sequence 1916, Ap
106	62	9.5	1471	7	US-11-174-307B-582	Sequence 582, App	179	60	9.1	3362	7	US-11-174-307B-2314	Sequence 2314, Ap
107	62	9.5	1542	7	US-11-174-307B-50	Sequence 50, App1	180	60	9.1	3499	7	US-11-063-439-96	Sequence 96, App1
108	62	9.5	1657	7	US-11-174-307B-112	Sequence 1212, Ap	181	60	9.1	3512	7	US-11-063-439-83	Sequence 83, App1
109	62	9.5	1929	7	US-11-174-307B-2462	Sequence 2462, Ap	182	60	9.1	3537	7	US-11-063-439-37	Sequence 37, App1
110	62	9.5	2052	7	US-11-174-307B-516	Sequence 516, App	183	60	9.1	3529	7	US-11-063-439-7	Sequence 35, App1
111	61.5	9.4	119	6	US-11-293-697-2647	Sequence 2647, A	184	59.5	9.1	120	7	US-11-075-891-35	Sequence 4652, Ap
112	61.5	9.4	143	6	US-10-449-902-29319	Sequence 29319, A	185	59.5	9.1	131	7	US-11-293-697-4652	Sequence 26974, A
113	61.5	9.4	210	7	US-11-293-697-2698	Sequence 2698, Ap	186	59.5	9.1	196	6	US-10-953-349-26924	Sequence 14634, A
114	61.5	9.4	254	7	US-11-075-891-10	Sequence 10, App1	187	59.5	9.1	240	7	US-11-056-355B-14634	Sequence 31333, A
115	61.5	9.4	254	7	US-11-075-891-16	Sequence 16, App1	188	59.5	9.1	247	6	US-10-449-902-31333	Sequence 31333, A
116	61.5	9.4	254	7	US-11-075-891-22	Sequence 22, App1	189	59.5	9.1	249	7	US-11-056-355B-14633	Sequence 14633, A
117	61.5	9.4	323	7	US-11-293-697-4057	Sequence 4057, Ap	190	59.5	9.1	292	7	US-11-056-355B-8565	Sequence 8565, Ap
118	61.5	9.4	348	6	US-10-449-902-51515	Sequence 51515, A	191	59.5	9.1	301	7	US-11-056-355B-8564	Sequence 8564, Ap
119	61.5	9.4	348	6	US-10-449-902-56016	Sequence 56016, A	192	59.5	9.1	396	6	US-10-449-902-35523	Sequence 35523, A
120	61.5	9.4	407	6	US-10-449-902-56016	Sequence 56016, A	193	59.5	9.1	433	6	US-10-449-902-31176	Sequence 31176, A
121	61.5	9.4	460	6	US-10-449-902-33081	Sequence 33081, A	194	59.5	9.1	453	6	US-10-449-902-53670	Sequence 53670, A
122	61.5	9.4	460	6	US-10-449-902-45508	Sequence 45508, A	195	59.5	9.1	470	7	US-11-056-355B-20257	Sequence 20257, A
123	61.5	9.4	1224	6	US-10-449-902-41406	Sequence 41406, A	196	59.5	9.1	485	6	US-10-449-902-46014	Sequence 46014, A
124	61.5	9.4	1298	7	US-11-174-307B-5050	Sequence 5050, Ap	197	59.5	9.1	587	6	US-10-449-902-45973	Sequence 45973, A
125	61.5	9.4	1574	7	US-11-174-307B-3200	Sequence 3200, Ap	198	59.5	9.1	785	7	US-11-174-307B-1002	Sequence 3002, Ap
126	61.5	9.4	1610	7	US-11-174-307B-1472	Sequence 1472, Ap	199	59.5	9.1	867	7	US-11-056-355B-87860	Sequence 87860, A
127	61.5	9.4	1925	7	US-11-174-307B-2362	Sequence 2362, Ap	200	59.5	9.1	892	7	US-11-056-355B-87859	Sequence 87859, A
128	61.5	9.4	2466	7	US-11-174-307B-2012	Sequence 2012, Ap	201	59.5	9.1	916	7	US-11-056-355B-87858	Sequence 87858, A
129	61.5	9.4	2416	7	US-11-174-307B-4660	Sequence 4660, Ap	202	59.5	9.1	935	7	US-11-056-355B-45271	Sequence 45271, A
130	61.5	9.4	3493	7	US-11-063-439-102	Sequence 103, App	203	59.5	9.1	959	7	US-11-056-355B-45270	Sequence 45270, A
131	61.5	9.4	3497	7	US-11-063-439-103	Sequence 102, App	204	59.5	9.1	998	7	US-11-056-355B-45269	Sequence 45269, A
132	61.5	9.3	247	7	US-11-293-697-2734	Sequence 2734, Ap	205	59.5	9.1	1215	7	US-11-174-307B-1632	Sequence 1632, Ap
133	61.5	9.3	439	6	US-10-449-902-35737	Sequence 35737, A	206	59.5	9.1	1324	7	US-11-174-307B-1210	Sequence 1210, Ap
134	61.5	9.3	868	6	US-10-449-902-56481	Sequence 56481, A	207	59.5	9.1	1374	7	US-11-174-307B-474	Sequence 474, App
135	61.5	9.3	1316	7	US-11-174-307B-588	Sequence 588, App	208	59.5	9.1	1463	7	US-11-174-307B-2526	Sequence 2526, Ap
136	61.5	9.3	1355	7	US-11-174-307B-2278	Sequence 2278, Ap	209	59.5	9.1	1766	7	US-11-174-307B-5194	Sequence 5194, Ap
137	61.5	9.3	1506	7	US-11-174-307B-4978	Sequence 4978, Ap	210	59.5	9.1	1897	7	US-11-174-307B-2884	Sequence 2884, Ap
138	61.5	9.3	1840	7	US-11-174-307B-1346	Sequence 1346, Ap	211	59.5	9.1	2228	7	US-11-174-307B-920	Sequence 920, App
139	61.5	9.3	2189	7	US-11-174-307B-3214	Sequence 3214, Ap	212	59.5	9.1	4709	7	US-11-174-307B-2292	Sequence 2292, Ap
140	61.5	9.3	2598	7	US-11-174-307B-488	Sequence 1488, Ap	213	59.5	9.0	88	6	US-10-449-902-46013	Sequence 46013, A
141	60.5	9.2	120	7	US-11-075-891-33	Sequence 33, App1	214	59.5	9.0	120	6	US-10-953-349-56061	Sequence 26061, A
142	60.5	9.2	120	7	US-11-075-891-34	Sequence 34, App1	215	59.5	9.0	126	7	US-11-056-355B-3751	Sequence 3751, Ap
143	60.5	9.2	352	7	US-11-056-355B-8196	Sequence 8196, Ap	216	59.5	9.0	225	7	US-11-197-712-193	Sequence 393, App
144	60.5	9.2	507	7	US-11-296-657-19	Sequence 19, App1	217	59.5	9.0	230	7	US-11-056-355B-71801	Sequence 71801, A
145	60.5	9.2	589	7	US-11-174-307B-4104	Sequence 4104, Ap	218	59.5	9.0	261	7	US-11-293-657-5513	Sequence 3553, Ap
146	60.5	9.2	689	7	US-11-174-307B-4500	Sequence 4500, Ap	219	59.5	9.0	318	7	US-11-056-355B-71800	Sequence 71800, A
147	60.5	9.2	728	6	US-10-504-973-10	Sequence 10, App1	220	59.5	9.0	319	6	US-10-449-902-47624	Sequence 47624, A
148	60.5	9.2	1501	7	US-11-174-307B-1648	Sequence 1648, Ap	221	59.5	9.0	418	7	US-11-056-355B-71799	Sequence 71799, A
149	60.5	9.2	1628	7	US-11-174-307B-2748	Sequence 2748, Ap	222	59.5	9.0	565	6	US-10-449-902-18750	Sequence 38750, A
150	60.5	9.2	2088	7	US-11-174-307B-4996	Sequence 4996, Ap	223	59.5	9.0	605	7	US-11-174-307B-5310	Sequence 5310, Ap
151	60.5	9.2	3460	6	US-10-505-928-104	Sequence 104, App	224	59.5	9.0	766	7	US-11-293-657-4088	Sequence 3088, Ap
152	60.5	9.1	91	6	US-10-449-902-36487	Sequence 36487, A	225	59.5	9.0	795	7	US-11-174-307B-1856	Sequence 1856, Ap
153	60.5	9.1	308	7	US-11-293-697-3870	Sequence 3870, Ap	226	59.5	9.0	983	7	US-11-174-307B-2434	Sequence 2434, Ap
154	60.5	9.1	485	6	US-10-449-902-37359	Sequence 37359, A	227	59.5	9.0	987	7	US-11-174-307B-236	Sequence 236, App
155	60.5	9.1	574	6	US-10-449-902-36659	Sequence 36659, A	228	59.5	9.0	999	7	US-11-174-307B-1422	Sequence 1422, Ap
156	60.5	9.1	713	6	US-11-056-355B-47272	Sequence 47272, A	229	59.5	9.0	1066	7	US-11-174-307B-1396	Sequence 1396, Ap
157	60.5	9.1	716	7	US-11-056-355B-47271	Sequence 47271, A	230	59.5	9.0	1098	7	US-11-174-307B-2006	Sequence 2006, Ap
158	60.5	9.1	752	7	US-11-056-355B-47270	Sequence 47270, A	231	59.5	9.0	1117	7	US-11-174-307B-1458	Sequence 1458, Ap
159	60.5	9.1	1006	6	US-10-449-902-41503	Sequence 41503, A	232	59.5	9.0	1148	7	US-11-247-437-6	Sequence 6, App1
160	60.5	9.1	1039	6	US-10-449-902-41129	Sequence 41129, A	233	59.5	9.0	1381	7	US-11-174-307B-3378	Sequence 3378, Ap
161	60.5	9.1	1153	7	US-11-174-307B-500	Sequence 500, App	234	59.5	9.0	1452	7	US-11-174-307B-4154	Sequence 4154, Ap
162	60.5	9.1	1170	7	US-11-174-307B-1300	Sequence 1300, Ap	235	59.5	9.0	1592	7	US-11-174-307B-5088	Sequence 5088, Ap
163	60.5	9.1	1187	7	US-11-174-307B-1728	Sequence 1728, Ap	236	59.5	9.0	1596	7	US-11-174-307B-792	Sequence 792, App
164	60.5	9.1	1310	6	US-10-449-902-41328	Sequence 41328, A	237	59.5	9.0	1937	7	US-11-174-307B-3074	Sequence 3074, Ap
165	60.5	9.1	1369	7	US-11-174-307B-2154	Sequence 2154, Ap	238	59.5	9.0	1962	7	US-11-174-307B-1748	Sequence 1748, Ap
166	60.5	9.1	1370	7	US-11-174-307B-2490	Sequence 2490, Ap	239	59.5	9.0	1962	7	US-11-174-307B-2754	Sequence 2754, Ap
167	60.5	9.1	1420	7	US-11-174-307B-2516	Sequence 2516, Ap	240	59.5	9.0	2101	7	US-11-174-307B-778	Sequence 778, App
168	60.5	9.1	1566	7	US-11-174-307B-2516	Sequence 2516, Ap	241	59.5	9.0	3494	7	US-11-063-439-50	Sequence 50, App1
169	60.5	9.1	1614	7	US-11-174-307B-1770	Sequence 1770, Ap	242	59.5	9.0	3503	7	US-11-063-439-23	Sequence 23, App1
170	60.5	9.1	1614	7	US-11-174-307B-1178	Sequence 1178, Ap	243	59.5	9.0	3512	7	US-11-063-439-72	Sequence 72, App1
171	60.5	9.1	1711	7	US-11-174-307B-2190	Sequence 2190, Ap	244	58.5	8.9	196	7	US-11-056-355B-18425	Sequence 18425, A
172	60.5	9.1	1753	7	US-11-174-307B-1198	Sequence 1198, Ap	245	58.5	8.9	202	7	US-11-056-355B-18424	Sequence 18424, A

OM protein - protein search, using sw model  
Run on: July 20, 2006, 09:50:42 ; Search time 83 Seconds  
(without alignments)  
661.036 Million cell updates/sec

Title: US-09-997-585-399  
Perfect score: 656  
Sequence: 1 MLPALPALVFTVAMSLA.....SAQLLCMPVGVARGALCQ 120  
BLOSUM62  
Scoring table: Gapop 10.0, Gapext 0.5  
2589679 segs, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: geneseqp1980s:\*  
A\_Geneseq\_8:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summaries

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV66754	standard;	protein;	120	AA.	
DE	Membrane-bound protein					PRO1187.
PN	WO963088-A2.					
PD	03-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 3;	Length 120;		
ID	AA24077	standard;	protein;	120	AA.	
DE	Human PRO1187					protein sequence SEQ ID NO:55.
PN	WO200053755-A2.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 3;	Length 120;		
ID	AA65277	standard;	protein;	120	AA.	
DE	Human PRO1187 (UN0601)					protein sequence SEQ ID NO:399.
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 4;	Length 120;		
ID	ABP6105	standard;	protein;	120	AA.	
DE	Human polypeptide					SEQ ID NO 1152.
PN	WO200270539-A2.					
PD	12-SEP-2002.					
PA	(HYSE-) HYSEQ INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 5;	Length 120;		
ID	AAU83640	standard;	protein;	120	AA.	
DE	Human PRO protein,					Seq ID No 98.
PN	WO200208288-A2.					
PD	31-JAN-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 5;	Length 120;		
ID	ADY31838	standard;	protein;	120	AA.	
DE	Novel human secreted and transmembrane protein					PRO1187.

PN	WO200193983-A1.					
PD	13-DEC-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 5;	Length 120;		
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ID	ABU58092	standard;	protein;	120	AA.	
DE	Human PRO polypeptide					#124.
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 8						
ID	ABU59170	standard;	protein;	120	AA.	
DE	Novel human secreted or transmembrane protein					PRO1187.
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 9						
ID	ABU82682	standard;	protein;	120	AA.	
DE	Human secreted/transmembrane protein					PRO1187.
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 10						
ID	ABU60601	standard;	protein;	120	AA.	
DE	Human secreted/transmembrane protein,					#160.
PN	US2002160384-A1.					
PD	31-OCT-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 11						
ID	ABU80787	standard;	protein;	120	AA.	
DE	Human PRO polypeptide					#49.
PN	US2003036635-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 12						
ID	ABO33753	standard;	protein;	120	AA.	
DE	Novel human secreted and transmembrane protein					PRO1187.
PN	US2003045687-A1.					
PD	06-MAR-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 13						
ID	ABU13983	standard;	protein;	120	AA.	
DE	Human PRO1187 polypeptide.					
PN	US2002103125-A1.					
PD	01-AUG-2002.					
PA	(GETH ) GENENTECH LTD.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 14						
ID	ABU72568	standard;	protein;	120	AA.	
DE	Novel human secreted and transmembrane protein					PRO1187.
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		
RESULT 15						
ID	ABU59317	standard;	protein;	120	AA.	
DE	Human secreted/transmembrane protein,					#160.
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 656;	DB 6;	Length 120;		

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Best Local Similarity 100.0%; Pred. No. 1.7e-67;
ID ABO26014 standard; protein; 120 AA.
DE Human PRO1187 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 17
ID ABU82096 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 18
ID ABUS9023 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #160.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 19
ID ABUS2401 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 20
ID ABUS9466 standard; protein; 120 AA.
DE Novel human secreted or transmembrane protein PRO1185.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 21
ID ABUS2232 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 22
ID ABUI0938 standard; protein; 120 AA.
DE Human PRO polypeptide #124.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 23
ID ABUS1690 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 24
ID ABUS8629 standard; protein; 120 AA.
DE Human secreted and transmembrane polypeptide PRO1187.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 25
ID ABO34143 standard; protein; 120 AA.
DE Human PRO1187 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 26
ID ABJ72276 standard; protein; 120 AA.
DE Human PRO1187 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 27
ID ADA37910 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 28
ID ADA21596 standard; protein; 120 AA.
DE Human secreted/transmembrane polypeptide PRO1187.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 29
ID ADA10383 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, PRO1187.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 30
ID ADA17927 standard; protein; 120 AA.
DE Human PRO1187 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 31
ID ADA28035 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 32
ID ADA94615 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003059632-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 33
ID ADA38840 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 34
ID ABJ72404 standard; protein; 120 AA.
DE Human PRO1187 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 35
ID ADA32961 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
```



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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:54:22 ; Search time 140 Seconds

(without alignments)  
792.871 Million cell updates/sec

Title: US-09-997-585-399

Perfect score: 656

Sequence: 1 MLPPALPPALVFTVAMSLA.....SAQLLCMPVGARGALCO 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 1500 summaries

Database : Uniprot 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	656	100.0	120	2	06UM09 HUMAN
2	85	13.0	638	2	03SID4 THIDA
3	83	12.7	502	2	09X8T8 STRCO
4	82.5	12.6	602	2	05JLX7 ORYSA
5	82.5	12.6	733	2	08L1Z0 ORYSA
6	82	12.4	741	2	02JDC2 PACTO
7	81.5	12.5	848	2	04GTES9 RALCO
8	80.5	12.3	371	2	073YK5 MYCPA
9	79.5	12.1	443	2	08D981 VIBVU
10	78.5	12.0	476	2	07ML91 VIBVU
11	78	11.9	156	2	05ZAG4 ORYSA
12	77.5	11.8	126	2	08LMB7 ORYSA
13	77.5	11.8	153	2	0339N8 ORYSA
14	77.5	11.8	246	2	06NKA1 CORDI
15	77.5	11.8	432	1	Y1S10 MYCTU
16	77.5	11.7	737	2	0802W8 BRARE
17	77	11.7	229	2	03JK00 BURPI
18	77	11.7	229	2	096440 LEICH
19	77	11.7	477	2	06NCK7 RHOPA
20	76.5	11.7	170	2	08M6E8 SCAND
21	76.5	11.7	195	2	02JTE6 PCYAN
22	76.5	11.7	259	2	06ZRH4 HUMAN
23	76	11.6	156	2	04MB72 ASPFU
24	76	11.6	379	2	04AQZ4 9BURK
25	76	11.6	1133	1	SRBP1 CRIGR
26	75.5	11.5	258	2	074MK0 NANEO
27	75.5	11.5	368	1	LIVE MYCLE
28	75.5	11.5	371	2	06NG91 CORDI
29	75	11.4	432	2	05P855 AZOSE
30	75	11.4	829	2	03FXU8 9DELT
31	75	11.4	927	2	Q2RPW4 RHORU

32	74.5	11.4	175	2	05X2P1 LERGA	05X2P1 Legionella
33	74.5	11.4	372	2	06OB43 METCA	06OB43 methylococ
34	74.5	11.4	835	1	BGAL LYCES	P48980 lycopersico
35	74.5	11.4	835	2	0546T5 LYCES	0546T5 lycopersico
36	74	11.3	176	2	05QKZ7 ANAPH	05QKZ7 anaplama p
37	74	11.3	317	2	07S9P9 NEUCR	07S9P9 neurospora
38	74	11.3	539	2	05NSO0 CRYNE	05NSO0 cryptococcu
39	74	11.3	790	2	034GL4 ORYSA	034GL4 oryza sativ
40	74	11.3	804	2	08ZRI6 STRAW	08ZRI6 streptomyc
41	74	11.3	2192	2	074F55 GEOSL	074F55 geobacter s
42	73.5	11.2	110	2	04CL01 TRYCR	04CL01 trypanosoma
43	73.5	11.2	381	2	03LZK8 SCAND	03LZK8 acrythosiph
44	73.5	11.2	390	2	09TIR0 BRAPS	09TIR0 bacterioph
45	73.5	11.2	433	2	07MEP5 VIBVU	07MEP5 vibrio vuln
46	73.5	11.2	433	2	08D7B6 VIBVU	08D7B6 vibrio vuln
47	73.5	11.2	440	2	047PM3 ANOGA	047PM3 anophelies g
48	73.5	11.2	854	2	047P80 THEFY	047P80 thermobifid
49	73.5	11.2	3649	2	083WE8 MICGR	083WE8 micromonop
50	73	11.1	136	2	099QD4 STRCO	099QD4 streptomyc
51	73	11.1	166	2	02RBD3 ORYSA	02RBD3 oryza sativ
52	73	11.1	202	2	03R2H1 XYLEA	03R2H1 xylella fas
53	73	11.1	224	2	08U9E7 AGRTS	08U9E7 agrobacteri
54	73	11.1	229	2	06ZBI4 BURMA	06ZBI4 burkholderi
55	73	11.1	229	2	063J63 BURPS	063J63 burkholderi
56	73	11.1	229	2	08PK02 XANAC	08PK02 xanthomonas
57	73	11.1	244	2	07CTA5 AGRTS	07CTA5 agrobacteri
58	72.5	11.1	325	2	07V835 PROMM	07V835 picrothoroco
59	72.5	11.1	339	2	08BIE5 MOUSE	08BIE5 mus musculu
60	72.5	11.1	355	2	032JL4 SHIDS	032JL4 shigella dy
61	72.5	11.1	359	2	0985C2 RHILLO	0985C2 rhizobium l
62	72.5	11.1	378	2	07UNU2 RHOPA	07UNU2 rhodospirill
63	72.5	11.1	477	2	088N51 PSERP	088N51 pseudomonas
64	72.5	11.1	3104	2	004846 CORAM	004846 corynebacte
65	72	11.0	159	2	09H233 PSSEAE	09H233 pseudomonas
66	72	11.0	247	2	03BSG0 XANCS	03BSG0 xanthomonas
67	72	11.0	386	2	098IX7 RHILLO	098IX7 rhizobium l
68	72	11.0	426	2	05NM74 ORYSA	05NM74 oryza sativ
69	72	11.0	540	2	05KCS5 CRYNE	05KCS5 cryptococcu
70	72	11.0	1063	1	SPTS YEAST	P27692 saccharomyc
71	71.5	10.9	144	2	04TIR8 TETNG	04TIR8 tetradon n
72	71.5	10.9	175	2	05ZM01 LEGPH	05ZM01 legionella
73	71.5	10.9	236	2	09Z4Z1 STRCO	09Z4Z1 streptomyc
74	71.5	10.9	267	2	03X2M5 PACTN	03X2M5 pseudobacter
75	71.5	10.9	272	2	08XRN3 RALSO	08XRN3 ralsconia s
76	71.5	10.9	418	2	043781 LOTJA	043781 lotus japon
77	71.5	10.9	748	2	03SWY0 9GAMM	03SWY0 shewanella
78	71.5	10.9	1128	2	05F488 CHICK	05F488 gallus galli
79	71	10.8	210	2	09RVL7 DEIRA	09RVL7 deinococcus
80	71	10.8	229	2	02TX77 BURTH	02TX77 burkholderi
81	71	10.8	266	2	06C6U2 YARLI	06C6U2 yarrowia li
82	71	10.8	268	2	04S483 TETNG	04S483 tetradon n
83	71	10.8	275	2	02XNL5 CHICK	02XNL5 gallus galli
84	71	10.8	283	1	Y393 IDILO	05T012 idiomarina
85	71	10.8	303	2	03FMD6 9BURK	03FMD6 geobacterax
86	71	10.8	321	2	057G10 SALCH	057G10 salmonella
87	71	10.8	321	2	08ZK75 SALTY	08ZK75 salmonella
88	71	10.8	342	2	08ZCW5 YERPE	08ZCW5 yersinia pe
89	71	10.8	381	2	04MCG6 ASPFU	04MCG6 aspergillus
90	71	10.8	405	2	02QSG8 ORYSA	02QSG8 oryza sativ
91	71	10.8	419	2	084NY5 ORYSA	084NY5 oryza sativ
92	71	10.8	450	2	07ZTX1 RYRIV	07ZTX1 ricinoderma
93	71	10.8	529	2	037TL0 SPHAN	037TL0 novosphingo
94	71	10.8	608	2	08KZT9 PSERU	08KZT9 pseudomonas
95	71	10.8	766	2	02RON5 ORYSA	02RON5 oryza sativ
96	71	10.8	4311	2	07YOK5 CANPA	07YOK5 canis famli
97	70.5	10.7	151	2	044BV3 CHRSL	044BV3 chronohalob
98	70.5	10.7	227	2	093783 HUMGT	093783 humicola gr
99	70.5	10.7	243	2	08PMI7 XANAC	08PMI7 xanthomonas
100	70.5	10.7	291	2	05GY57 XANOR	05GY57 xanthomonas
101	70.5	10.7	368	1	LIVE MYCTU	Q5739 mycobacteri
102	70.5	10.7	370	2	07TYX3 MYCBO	07TYX3 mycobacteri
103	70.5	10.7	370	2	080V44 MOUSE	080V44 mus musculu
104	70.5	10.7	410	2	04KA26 PSERS	04KA26 pseudomonas

105	70.5	10.7	418	2	02XIP7_PSEBU	02XIP7_pseudomonas	178	69	10.5	940	2	04WJP5_ASFPV	04WJP5_aspergillus
106	70.5	10.7	418	2	088IK5_PSEBK	088IK5_pseudomonas	179	69	10.5	1024	2	SRBP1_RAT	P56720 rattus norv
107	70.5	10.7	419	2	07GIG6_SOIBN	07GIG6_glycine max	180	69	10.5	1134	1	SRBP1_MOUSE	09wnc mus musculu
108	70.5	10.7	420	2	040107_LUPAN	040107_lupinus ang	181	69	10.5	1173	2	03VGI0_RHOPA	037910 rhodopseudo
109	70.5	10.7	420	2	040108_LUPAN	040108_lupinus ang	182	69	10.5	1234	2	09HPM2_HALISA	09HPM2_halobacteri
110	70.5	10.7	421	2	07NJY7_GLOVAT	07NJY7_gloeobacter	183	69	10.5	1501	2	06JMR3_BURPS	06JMR3_burkholderi
111	70.5	10.7	426	2	048548_SOYBN	048548_glycine max	184	69	10.5	1511	2	03JGR2_BURP1	03JGR2_burkholderi
112	70.5	10.7	477	2	03UD59_MOUSE	03UD59_mus musculu	185	69	10.5	1607	2	07OHZ9_9ACTO	07OHZ9_streptomyce
113	70.5	10.7	513	2	046334_9BUNK	046334_comamonas s	186	69	10.5	1960	2	064HK8_9ACTO	064HK8_streptomyce
114	70.5	10.7	521	2	03TQF5_MOUSE	03TQF5_mus musculu	187	69	10.5	2184	2	04P5V6_9ACTO	04P5V6_ustilago ma
115	70.5	10.7	535	2	06EUF2_ORYSA	06EUF2_oryza sativ	188	69	10.5	3500	2	070100_9ACTO	070100_9ACTO
116	70.5	10.7	559	2	03TR84_MOUSE	03TR84_mus musculu	189	68.5	10.4	189	2	07ULV6_RHOBA	07ULV6_rhodopirell
117	70.5	10.7	591	2	0913V3_PSEAE	0913V3_pseudomonas	190	68.5	10.4	281	2	07NT57_CHRVO	07NT57_chromobacte
118	70.5	10.7	684	2	035C98_9BRAD	035C98_bradyrhizob	191	68.5	10.4	291	2	02IXJ3_RHOPA	02IXJ3_rhodopseudo
119	70.5	10.7	738	2	05R8K5_PONPY	05R8K5_pongo pygma	192	68.5	10.4	306	2	05IGM8_9CAUD	05IGM8_bacteriopia
120	70.5	10.7	777	2	06PAS9_MOUSE	06PAS9_mus musculu	193	68.5	10.4	464	2	06XMY6_RHOER	06XMY6_rhodococcus
121	70.5	10.7	1005	2	03TEB3_MOUSE	03TEB3_mus musculu	194	68.5	10.4	502	2	04P717_USTMA	04P717_ustilago ma
122	70.5	10.7	1005	2	08BLR5_MOUSE	08BLR5_m 10 days n	195	68.5	10.4	513	2	024719_COMTE	024719_comamonas t
123	70.5	10.7	1046	2	038119_9TRYR	038119_rypanosoma	196	68.5	10.4	551	2	09BN27_RHIL0	09BN27_rhizobium l
124	70.5	10.7	1441	2	080TF2_MOUSE	080TF2_mus musculu	197	68.5	10.4	610	2	02TXM7_ASFOR	02TXM7_aspergillus
125	70.5	10.7	2038	2	05RPF0_MOUSE	05RPF0_mus musculu	198	68.5	10.4	732	2	02GOV0_ORYSA	02GOV0_oryza sativ
126	70	10.7	206	2	08ZSQ6_PYRAE	08ZSQ6_pyrobaculum	199	68.5	10.4	748	2	08ECT4_SHEON	08ECT4_shewanella
127	70	10.7	321	2	05PJ70_SALPA	05PJ70_salmonella	200	68.5	10.4	931	2	04KAL5_PSEFS	04KAL5_pseudomonas
128	70	10.7	321	2	08Z156_SALPA	08Z156_salmonella	201	68.5	10.4	1106	2	04FY01_LBIMA	04FY01_leishmania
129	70	10.7	416	2	07XGV9_ORYSA	07XGV9_oryza sativ	202	68	10.4	230	2	04IG74_GIBZE	04IG74_gibberella
130	70	10.7	416	2	094HT1_ORYSA	094HT1_oryza sativ	203	68	10.4	287	2	0855F3_9CAUD	0855F3_mycobacteri
131	70	10.7	445	2	04NRG7_9MTCB	04NRG7_arthrobacte	204	68	10.4	361	2	03BVB2_XANCS	03BVB2_xanthomonas
132	70	10.7	469	2	03QGA0_9RHOB	03QGA0_silicibacte	205	68	10.4	378	2	04S920_TITNG	04S920_tetradodon n
133	70	10.7	478	2	09A9V9_CAUCR	09A9V9_caulobacter	206	68	10.4	409	2	043QNT_SOLUS	043QNT_solibacter
134	70	10.7	537	2	02J561_9ACTO	02J561_franksia sp.	207	68	10.4	432	1	PURAI_CHRVO	070971 chromobacte
135	70	10.7	598	1	PANK1_HUMAN	08E04_homo sapien	208	68	10.4	524	2	04CYE1_TRYCR	04CYE1_cryptosoma
136	70	10.7	778	2	05BAM2_EMENT	05BAM2_aspergillus	209	68	10.4	581	1	SYR_BORBU	053538 mycobacteri
137	70	10.7	949	2	04TK25_THERY	04TK25_thermobifid	210	68	10.4	592	2	05J538_MYCTU	05J538_mycobacteri
138	70	10.7	1646	2	07WTE3_9ACTO	07WTE3_aspergillu	211	68	10.4	592	2	07WEM4_MYCTU	07WEM4_mycobacteri
139	69.5	10.6	154	2	02UUB4_ASFOR	02UUB4_aspergillus	212	68	10.4	663	2	03TYX1_MOUSE	03TYX1_mus musculu
140	69.5	10.6	220	2	069LP6_ORYSA	069LP6_oryza sativ	213	68	10.4	697	2	08BU52_XANCS	08BU52_xanthomonas
141	69.5	10.6	220	2	08KRF6_CHLTE	08KRF6_chloridium	214	68	10.4	697	2	08PL70_XANAC	08PL70_xanthomonas
142	69.5	10.6	224	2	06H8H2_ORYSA	06H8H2_oryza sativ	215	68	10.4	-778	2	07XOR8_ORYSA	07XOR8_oryza sativ
143	69.5	10.6	247	2	084T14_ARATH	084T14_arabidopsis	216	68	10.4	866	2	0502N3_BRARE	0502N3_brachydanio
144	69.5	10.6	247	2	09LNM6_ARATH	09LNM6_arabidopsis	217	68	10.4	866	2	09JUKT_MOUSE	09JUKT_mus musculu
145	69.5	10.6	345	1	YKCO_CABEL	P42001_caeonornabdi	218	68	10.4	1022	2	05SRX5_MOUSE	05SRX5_mus musculu
146	69.5	10.6	345	2	09X7U8_STRCO	09X7U8_streptomyce	219	68	10.4	1069	2	03U458_MOUSE	03U458_mus musculu
147	69.5	10.6	380	2	08ZNO5_STRAM	08ZNO5_atreptomyce	220	68	10.4	1075	2	05GRX6_MOUSE	05GRX6_mus musculu
148	69.5	10.6	418	1	AAAT1_MEDSA	P28011_medicago sa	221	68	10.4	1078	2	07NMW9_CHRVO	07NMW9_chromobacte
149	69.5	10.6	535	1	1897_MYCTU	P64751_mycobacteri	222	68	10.4	1134	2	03UDJ3_MOUSE	03UDJ3_mus musculu
150	69.5	10.6	535	1	Y921_MYCBO	P64752_mycobacteri	223	68	10.4	1134	2	08CTJ3_MOUSE	08CTJ3_mus musculu
151	69.5	10.6	738	1	PIOD3_HUMAN	060568_homo sapien	224	68	10.4	1240	2	04Q0V2_LETMA	04Q0V2_leishmania
152	69.5	10.6	738	2	PIOD3_PONPY	05R6H5_pongo pygma	225	68	10.4	1384	1	CNTP1_HUMAN	P78357 homo sapien
153	69.5	10.6	857	2	03GVH5_9ACTO	03GVH5_nocardioide	226	68	10.4	2024	2	09EMW3_9ACTO	09EMW3_streptomyce
154	69.5	10.6	908	2	05B3J7_EMENT	05B3J7_aspergillus	227	68	10.4	2430	2	060WZ3_CABER	060WZ3_caeonornabdi
155	69	10.5	121	2	07HTG6_MOUSE	07HTG6_m 4 days ne	228	67.5	10.3	91	2	0303P5_SRRSU	0303P5_streptococc
156	69	10.5	160	2	07W7X3_BORPA	07W7X3_bordetella	229	67.5	10.3	206	2	0447F5_SOLUS	0447F5_solibacter
157	69	10.5	160	2	07WLB3_BORBR	07WLB3_bordetella	230	67.5	10.3	211	2	04SVU9_PABPO	04SVU9_paeibacill
158	69	10.5	178	2	06ES44_ORYSA	06ES44_oryza sativ	231	67.5	10.3	227	2	06Z8Q7_ORYSA	06Z8Q7_oryza sativ
159	69	10.5	229	2	02P2C6_XANOR	02P2C6_xanthomonas	232	67.5	10.3	256	2	031LV8_SYNP7	031LV8_synecchococ
160	69	10.5	229	2	05GZB7_XANOR	05GZB7_xanthomonas	233	67.5	10.3	256	2	05N017_SYNP6	05N017_synecchococ
161	69	10.5	262	2	034T69_9GAMM	034T69_alkalilimna	234	67.5	10.3	342	2	09RUU0_DEIRA	09RUU0_deinococcus
162	69	10.5	319	2	08RIH2_MOUSE	08RIH2_mus musculu	235	67.5	10.3	345	2	09WZ54_HUMAN	09WZ54_homo sapien
163	69	10.5	342	2	066BD1_YERPS	066BD1_yersinia ps	236	67.5	10.3	361	2	06X3X7_IPOPI	06X3X7_ipomoea ntl
164	69	10.5	348	2	04SEN8_TETNG	04SEN8_tetradodon n	237	67.5	10.3	361	2	06X3X8_IPOHI	06X3X8_ipomoea hed
165	69	10.5	381	2	03XT41_9PROT	03XT41_magnetococ	238	67.5	10.3	361	2	06X3Y0_IPOHE	06X3Y0_ipomoea hed
166	69	10.5	416	2	03MMH2_9RHIZ	03MMH2_mesorhizobi	239	67.5	10.3	369	2	006055_MYCGO	006055_mycobacteri
167	69	10.5	466	2	093785_TRITE	093785_mesorhizoma	240	67.5	10.3	389	2	03AV73_SYNS9	03AV73_synecchococ
168	69	10.5	466	2	066PFP_FRAAN	066PFP_fragaria an	241	67.5	10.3	391	2	04JWDS_CORJK	04JWDS_corynebacte
169	69	10.5	468	2	P96444_RHIME	P96444_rhizobium m	242	67.5	10.3	393	2	08RY22_STRCU	08RY22_streptomyce
170	69	10.5	484	2	04DKB8_TRYCR	04DKB8_rypanosoma	243	67.5	10.3	405	2	05H910_HUMAN	05H910_homo sapien
171	69	10.5	546	2	08CJN9_STRCO	08CJN9_streptomyce	244	67.5	10.3	420	2	022603_IPOPU	022603_ipomoea pur
172	69	10.5	547	2	03AIM3_SYNSC	03AIM3_synecchococ	245	67.5	10.3	452	2	04WR02_ASFPV	04WR02_aspergillus
173	69	10.5	705	2	096B28_HUMAN	096B28_homo sapien	246	67.5	10.3	477	2	02X8E3_PSEPU	02X8E3_pseudomonas
174	69	10.5	709	2	05XIFY1_BRARE	05XIFY1_brachydanio	247	67.5	10.3	490	2	033TR7_9GAMM	033TR7_shewanella
175	69	10.5	729	2	090ZN6_BRARE	090ZN6_brachydanio	248	67.5	10.3	527	2	09PUH8_ARATH	09PUH8_arabidopsis
176	69	10.5	893	2	03HYA0_9PSED	03HYA0_pseudomonas	249	67.5	10.3	658	2	05AR18_EMENT	05AR18_aspergillus
177	69	10.5	893	2	092V32_RHIME	092V32_rhizobium m	250	67.5	10.3	674	2	070KCI_9ACTO	070KCI_gordonia we